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**RAW SEQUENCE LISTING** DATE: 11/26/2001  
**PATENT APPLICATION:** US/09/848,915A TIME: 12:17:13

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TIME: 12:17:13

Input Set : N:\Crf3\RULE60\09848915A.txt  
Output Set: N:\CRF3\11262001\I848915A.raw

## **SEQUENCE LISTING**

C--> 5 (1) GENERAL INFORMATION:  
7 (i) APPLICANT: Hillman, Jennifer L.  
8 Goli, Surya K.  
C--> 10 (ii) TITLE OF INVENTION: NOVEL TUMORIGENESIS PROTEIN  
12 (iii) NUMBER OF SEQUENCES: 3  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
16 (B) STREET: 3174 Porter Drive  
17 (C) CITY: Palo Alto  
18 (D) STATE: CA  
19 (E) COUNTRY: USA  
20 (F) ZIP: 94304  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Diskette  
24 (B) COMPUTER: IBM Compatible  
25 (C) OPERATING SYSTEM: DOS  
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
28 (vi) CURRENT APPLICATION DATA:  
29 (A) APPLICATION NUMBER: US/09/848,915A  
C--> 30 (B) FILING DATE: 04-May-2001  
31 (C) CLASSIFICATION:  
33 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: 09/183,825  
35 (B) FILING DATE: 1998-10-30  
38 (viii) ATTORNEY/AGENT INFORMATION:  
39 (A) NAME: Billings, Lucy J.  
40 (B) REGISTRATION NUMBER: 36,749  
41 (C) REFERENCE/DOCKET NUMBER: PF-0247 US  
43 (ix) TELECOMMUNICATION INFORMATION:  
44 (A) TELEPHONE: 415-855-0555  
45 (B) TELEFAX: 415-845-4166  
46 (C) TELEX:  
49 (2) INFORMATION FOR SEQ ID NO: 1:  
51 (i) SEQUENCE CHARACTERISTICS:  
52 (A) LENGTH: 195 amino acids  
53 (B) TYPE: amino acid  
54 (C) STRANDEDNESS: single  
55 (D) TOPOLOGY: linear  
57 (vii) IMMEDIATE SOURCE:  
58 (A) LIBRARY: UTRSNOT02  
59 (B) CLONE: 2267574  
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
63 Met Glu Leu Ser Glu Ser Val Gln Lys Gly Phe Gln Met Le  
64 1 5 10  
65 Pro Arg Ser Phe Asp Ser Asn Ala Phe Thr Leu Leu Leu Ar  
66 20 25 30

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67 Phe Gln Ser Leu Leu Asp Ala Gln Ala Asp Glu Ala Val Leu Asp His  
68 35 40 45  
69 Pro Asp Leu Lys His Ile Asp Pro Val Val Leu Lys His Cys His Ala  
70 50 55 60  
71 Ala Ala Ala Thr Tyr Ile Leu Glu Ala Gly Lys His Arg Ala Asp Lys  
72 65 70 75 80  
73 Ser Thr Leu Ser Thr Tyr Leu Glu Asp Cys Lys Phe Asp Arg Glu Arg  
74 85 90 95  
75 Ile Glu Leu Phe Cys Thr Glu Tyr Gln Asn Asn Lys Asn Ser Leu Glu  
76 100 105 110  
77 Ile Leu Leu Gly Ser Ile Gly Arg Ser Leu Pro His Ile Thr Asp Val  
78 115 120 125  
79 Ser Trp Arg Leu Glu Tyr Gln Ile Lys Thr Asn Gln Leu His Arg Met  
80 130 135 140  
81 Tyr Arg Pro Ala Tyr Leu Val Thr Leu Ser Val Gln Asn Thr Asp Ser  
82 145 150 155 160  
83 Pro Ser Tyr Pro Glu Ile Ser Phe Ser Cys Ser Met Glu Gln Leu Gln  
84 165 170 175  
85 Asp Leu Val Gly Lys Leu Lys Asp Ala Ser Lys Ser Leu Glu Arg Ala  
86 180 185 190

87 Thr Gln Leu  
88 195

90 (2) INFORMATION FOR SEQ ID NO: 2:

92 (i) SEQUENCE CHARACTERISTICS:  
93 (A) LENGTH: 751 base pairs  
94 (B) TYPE: nucleic acid  
95 (C) STRANDEDNESS: single  
96 (D) TOPOLOGY: linear

98 (vii) IMMEDIATE SOURCE:

99 (A) LIBRARY: UTRSNOT02  
100 (B) CLONE: 2267574

102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

104 CGAACGTACG GCGCGCTCAC AATGGAGCTC TCGGAGTCTG TGCAGAAAGG CTTCCAGATG	60
105 CTGGCGGATC CCCGCTCCTT CGACTCCAAC GCCTTCACGC TTCTCCTCCG GCGGGCATTC	120
106 CAGAGTCTGC TGGACGCCA GGC GGACGAG GCCGTGTTAG ATCATCCAGA CTGAAACAT	180
107 ATCGACCCAG TGGTTTAAAC ACATTGTCA GCAGCAGCTG CAACTTACAT ACTAGAGGCA	240
108 GGAAAGCACC GAGCTGACAA GTCAACTCTA AGCACTTATC TAGAAGACTG TAAATTGAC	300
109 AGAGAGCGAA TAGAACTGTT TTGCACCGAA TATCAGAATA ATAAGAATTG CCTAGAAATC	360
110 CTACTGGGAA GTATAGGCAG ATCTCTCCCT CATATAACGG ATGTTTCTTG GCGCTTGGAA	420
111 TATCAGATAA AGACCAATCA ACTTCATAGG ATGTACAGAC CTGCATATTT GGTGACCTTA	480
112 AGTGTACAGA ACACGTGATTC CCCATCCTAT CCAGAGATTA GTTTTAGTTG CAGCATGGAA	540
113 CAATTACAGG ACTTGGTGGG GAAACTTAAA GATGCTTCGA AAAGCCTGGA AAGAGCAACT	600
114 CAGTTGTAAC TTGGGAAAGT TAACGATCCG CCCGAGTGCA GAGGAAAACC AGAAACGCCT	660
115 TGCCCTTCAGC TGAACCACCG TTTGTGCGAG CTGGATGTCC TTTTCAGTAG AAAAGAATT	720
116 TCCTTTTGAA TTTATACCAT TCANCAATT T	751

118 (2) INFORMATION FOR SEQ ID NO: 3:

120 (i) SEQUENCE CHARACTERISTICS:  
121 (A) LENGTH: 195 amino acids  
122 (B) TYPE: amino acid

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123                   (C) STRANDEDNESS: single  
124                   (D) TOPOLOGY: linear  
126       (vii) IMMEDIATE SOURCE:  
127               (A) LIBRARY: GenBank  
128               (B) CLONE: 265569  
130       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
132 Met Glu Leu Ser Glu Ser Val Gln Arg Gly Ile Gln Thr Leu Ala Asp  
133       1               5               10               15  
134 Pro Gly Ser Phe Asp Ser Asn Ala Phe Ala Leu Leu Leu Arg Ala Ala  
135       20              25              30  
136 Phe Gln Ser Leu Leu Asp Ala Arg Ala Asp Glu Ala Ala Leu Asp His  
137       35              40              45  
138 Pro Tyr Leu Lys Gln Ile Asp Pro Val Val Leu Lys His Cys His Ala  
139       50              55              60  
140 Ala Ala Ala Thr Cys Ile Leu Glu Ala Gly Lys His Gln Val Asp Lys  
141       65              70              75              80  
142 Ser Thr Leu Ser Thr Tyr Leu Glu Asp Cys Lys Phe Asp Arg Glu Arg  
143       85              90              95  
144 Ile Glu Leu Phe Cys Thr Glu Tyr Gln Asn Asn Lys Asn Ser Leu Glu  
145       100             105             110  
146 Thr Leu Leu Gly Ser Ile Gly Arg Ser Leu Pro His Ile Thr Asp Val  
147       115             120             125  
148 Ser Trp Arg Leu Glu Tyr Gln Ile Lys Thr Asn Gln Leu His Lys Met  
149       130             135             140  
150 Tyr Arg Pro Gly Tyr Leu Val Thr Leu Asn Val Glu Asn Asn Asp Ser  
151       145             150             155             160  
152 Gln Ser Tyr Pro Glu Ile Asn Phe Ser Cys Asn Met Glu Gln Leu Gln  
153       165             170             175  
154 Asp Leu Val Gly Lys Leu Lys Asp Ala Ser Lys Ser Leu Glu Arg Ala  
155       180             185             190  
156 Thr Gln Leu  
157       195

VERIFICATION SUMMARY

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L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]  
L:10 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]